

# SEQUENCE LISTING

<110> Maines, Mahin D.

<120> METHODS OF MODIFYING CELL STRUCTURE AND REMODELING  
TISSUE

<130> 176/60981

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<150> 60/261,500

<151> 2001-01-12

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

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<212> PRT

<213> Homo sapiens

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Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro

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Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu

35 40 45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser

50 55 60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His

65 70 75 80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val

85 90 95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu

100 105 110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu

115 120 125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp  
130 135 140

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp  
145 150 155 160

Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu  
165 170 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu  
180 185 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu  
195 200 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys  
210 215 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn  
225 230 235 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn  
245 250 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala  
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Gln Lys Tyr Cys Cys Ser Arg Lys  
290 295

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<212> DNA

<213> Homo. sapiens

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tccgtgcgga tgagggactt gcggaatcca cacccttcct cagcgttcct gaacctgatt 180

ggcttcgtgt cgagaaggga gctcgggagc attgatggag tccagcagat ttctttggag 240

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<210> 3
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Met Asn Thr Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
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Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
20 25 30

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Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
35 40 45

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Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
50 55 60

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Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
65 70 75 80

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Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
85 90 95

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Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
100 105 110

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Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
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Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
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Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
145 150 155 160

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..... 180 ..... 185 ..... 190 .....
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..... Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu .....
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..... Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys .....
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..... Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala .....
..... 260 ..... 265 ..... 270 .....
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..... Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile .....
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..... 20 ..... 25 ..... 30 .....
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..... Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly .....
..... 35 ..... 40 ..... 45 .....
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..... Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser .....
..... 50 ..... 55 ..... 60 .....
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..... Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu .....

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Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu			
100	105	110	
Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu			
115	120	125	
Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu			
130	135	140	
Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg			
145	150	155	160
Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val			
165	170	175	
Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg			
180	185	190	
Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn			
195	200	205	
Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg			
210	215	220	
Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val			
225	230	235	240
Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile			
245	250	255	
Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala			
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Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln			
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Lys Leu Cys His Gln Lys Lys			
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<223> where X is any aa

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Phe Xaa Val Val Val Val

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<210> 7

<211> 6

<212> PRT

<213> Artificial Sequence

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binding domain of BVR .....

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<223> where X is any aa .....

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Gly Xaa Gly Xaa Xaa Gly .....  
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<211> 8 .....  
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<213> Artificial Sequence .....

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<223> Description of Artificial Sequence: .....  
oxidoreductase domain of BVR .....

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zipper of BVR .....

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Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu  
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<212> PRT  
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Ser Arg Arg  
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<210> 11  
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<223> Description of Artificial Sequence: kinase motif  
of BVR

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Lys Gly Ser  
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<223> Description of Artificial Sequence: methylation  
site of BVR

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